

ATGAGAAGGTGAGAATAAGTGGGAGGCCCGGCGCCCCCGGTGTCCCCGCCAGGCC  
MetArgArgCysArgIleSerGlyArgProProAlaProProGlyValProAlaGlnAla  
CCTGTCTCCCAGCCTGATGCCCTGGCCACCAGAGGAAAGTGGTGTCACTGGATAGATGTG  
ProValSerGlnProAspAlaProGlyHisGlnArgLysValValSerTrpIleAspVal  
TATACTCGCGCTACCTGCCAGCCCCGGGAGGTGGTGGTGCCTTGACTGTGGAGCTCATG  
TyrThrArgAlaThrCysGlnProArgGluValValValProLeuThrValGluLeuMet  
GGCACCGTGGCAAACAGCTGGTGCCCAGCTGCGTGACTGTGCAGCGCTGGTGGCTGC  
GlyThrValAlaLysGlnLeuValProSerCysValThrValGlnArgCysGlyGlyCys  
TGCCCTGACGATGGCCTGGAGTGTCGCCCAGGGCAGCACCAAGTCCGGATGCAGATC  
CysProAspAspGlyLeuGluCysValProThrGlyGlnHisGlnValArgMetGlnIle  
CTCATGATCCGGTACCCGAGCAGTCAGCTGGGGAGATGTCCCTGGAAGAACACAGCCAG  
LeuMetIleArgTyrProSerSerGlnLeuGlyGluMetSerLeuGluGluHisSerGln  
TGTGAATGCAGACCTAAAAAAAGGACAGTGCTGTGAAGCCAGACAGGGCTGCTACTCCC  
CysGluCysArgProLysLysAspSerAlaValLysProAspArgAlaAlaThrPro  
CACCAACCGTCCCCAGCCCCGTTCTGTTCCGGGCTGGACTCTGCCCGGAGCACCCCTCC  
HisHisArgProGlnProArgSerValProGlyTrpAspSerAlaProGlyAlaProSer  
CCAGCTGACATACCCAAATCCCACTCCAGCCCCAGGCCCTCTGCCCACGCTGCACCCAG  
ProAlaAspIleThrGlnSerHisSerProArgProLeuCysProArgCysThrGln  
CACCAACCGTGCCTGACCCCCGGACCTGCCGCTGCCGCTGTCGACGCCAGCTTCCTC  
HisHisGlnCysProAspProArgThrCysArgCysArgCysArgArgSerPheLeu  
CGTTGTCAAGGGCGGGCTTAGAGCTAACCCAGACACCTGCAGGTGCCGGAAGCTGCGA  
ArgCysGlnGlyArgGlyLeuGluLeuAsnProAspThrCysArgCysArgLysLeuArg  
AGGTGA  
ArgEnd

FIGURE 1 11

|  |     |     |     |     |     |
|--|-----|-----|-----|-----|-----|
| 10   | 20  | 30  | 40  | 50  |     |
| MNFLLSWVHWSLALLYLHHAKWSQAAPMAEGGGQNHH-EVVKFMDVYQRSYC         |     |     |     |     |     |
| :: :: :: :: :: :: ::   |     |     |     |     |     |
| MRRCRISGRPPAPPGVPAQAPVSQPDAPGHQRKVWSWIDVYTRATC               |     |     |     |     |     |
|  |     |     |     |     |     |
| 60   | 70  | 80  | 90  | 100 | 110 |
| HPIETLVDIFQEYPDEIEYIFPKPSCVPLMRCGGCCNDEGLECVPTESNITMQIMRIKPH |     |     |     |     |     |
| :: :: :: :: :: ::  |     |     |     |     |     |
| QPREVVVPLTVELMGTVAKQLVPSCTVQRCGGCPDDGLECVPTGQHQVRMQLMIR-Y    |     |     |     |     |     |
|  |     |     |     |     |     |
| 120  | 130 | 140 | 150 | 160 |     |
| QQQHIGEMSFLQHNKCBCRPKK-----DRA----RQEKKSVRGKGKGQKRKRKKSRY    |     |     |     |     |     |
| :: :: :: :: ::   |     |     |     |     |     |
| PSSQLGEMSLEEHHSQCECRPKKDSAVKPDRAATPHIRPQPRSVPGWDSAPGAPSPADIT |     |     |     |     |     |
|  |     |     |     |     |     |
| 170  | 180 | 190 | 200 | 210 |     |
| KSWSVPCGPCSERRKHLFVQDPQTCKCSCCKNTD-SRCKARQLELNERTCRCDKPRR    |     |     |     |     |     |
| :: :: :: :: ::   |     |     |     |     |     |
| QSHSSPRPLCPRCTQHHQCPDPRTCRCRRRSFLRCQGRGLELNPDTCRCKLRR        |     |     |     |     |     |

Figure 2. Sequence alignment of VEGF3 (lower line) compared to VEGF from human (upper line).

FIGURE 2 11